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#4

120> TITLE OF INVENTION: CARBAMOYL-PHOSPHATE SYNTHETASE GENE OF CORYNEFORM
BACTERIA AND METHOD FOR PRODUCING L-ARGININE
130> FILE REFERENCE: OP945CIP
140> CURRENT APPLICATION NUMBER: US/09/629,616
141> CURRENT FILING DATE: 2000-07-31
160> NUMBER OF SEQ ID NOS: 7
170> SOFTWARE: PatentIn Ver. 2.0

210> SEQ ID NO 1
211> LENGTH: 4837
212> TYPE: DNA
213> ORGANISM: Brevibacterium lactofermentum
220> FEATURE:
221> NAME/KEY: CDS
222> LOCATION: (283)..(1461)
221> NAME/KEY: CDS
222> LOCATION: (1470)..(4808)
400> SEQUENCE: 1

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Ile Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr Ala Met Thr Gly
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Tyr Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg Gln Ile Val Val
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Phe Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu Leu Val Glu Ile
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Val Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu Ser Val Glu Val
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Ser Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly Glu Glu Arg His
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Thr Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn Thr Pro Arg Arg						
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ttc tct gca cgc ggt gtt cgc acc gtc atc gtg cct gct gaa acc cca						966
Phe Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro Ala Glu Thr Pro						
	215		220		225	
ttg gag gac atc aag cag tac aac cca tca ggc gtg ttt atc tcc aat						1014
Leu Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val Phe Ile Ser Asn						
	230		235		240	
ggc cct ggc gac cct gca gca gca gac gtc atg gtt gat atc gtc cgc						1062
Gly Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val Asp Ile Val Arg						
	245		250		255	260
gaa gtt ctg gaa gcc gac att cca ttc ttt ggc atc tgc ttc ggc aac						1110
Glu Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile Cys Phe Gly Asn						
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cag atc ctc ggc cgc gca ttc ggc atg gag acc tac aag ctg aag ttc						1158
Gln Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr Lys Leu Lys Phe						
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ggc cac cgc ggc atc aac gtt cca gtg aag aag cac atc acc ggc aag						1206
Gly His Arg Gly Ile Asn Val Pro Val Lys Asn His Ile Thr Gly Lys						
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atc gac atc acc gcc cag aac cac ggc ttc gca ctc aag ggt gaa gca						1254
Ile Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu Lys Gly Glu Ala						
	310		315		320	
ggc cag gaa ttc gag aca gat ttc ggc act gcg att gtc acc cac acc						1302
Gly Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile Val Thr His Thr						
	325		330		335	340
tgc ctt aac gac ggc gtc gtt gaa ggt gtt gcg ctg aag tcc gga cgc						1350
Cys Leu Asn Asp Gly Val Val Glu Gly Val Ala Leu Lys Ser Gly Arg						
	345		350		355	
gca tac tcc gtt cag tac cac cca gag gcc gct gcc ggc cca aat gat						1398
Ala Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala Gly Pro Asn Asp						
	360		365		370	
gca agc ccc ctg ttt gac cag ttt gtt gag ctg atg gat gca gac gct						1446
Ala Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met Asp Ala Asp Ala						
	375		380		385	
cag aag aaa ggc gca taaataac atg cca aag cgt tca gat att aac cac						1496
Gln Lys Lys Gly Ala Met Pro Lys Arg Ser Asp Ile Asn His						
	390		1		5	
gtc ctc gtc atc ggt tcc ggc ccc atc gtc att ggc cag gca tgt gaa						1544
Val Leu Val Ile Gly Ser Gly Pro Ile Val Ile Gly Gln Ala Cys Glu						
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ttc gac tac tcc ggc acc cag gct tgc cgc gtg ctg aag gaa gag gga						1592
Phe Asp Tyr Ser Gly Thr Gln Ala Cys Arg Val Leu Lys Glu Glu Gly						
	30		35		40	
ctg cgc gtc acc ctc atc aac tcc aac cca gca acg atc atg acc gac						1640
Leu Arg Val Thr Leu Ile Asn Ser Asn Pro Ala Thr Ile Met Thr Asp						
	45		50		55	
cca gaa atg gct gac cac acc tac gtg gag cca atc gag ccg gaa tac						1688
Pro Glu Met Ala Asp His Thr Tyr Val Glu Pro Ile Glu Pro Glu Tyr						
	60		65		70	
atc gac aag att ttc gct aag gag atc gag cag ggc cac cca atc gac						1736
Ile Asp Lys Ile Phe Ala Lys Glu Ile Glu Gln Gly His Pro Ile Asp						
	75		80		85	
gcc gtc ctg gca acc ctt ggt ggc cag act gca ctt aac gca gct atc						1784
Ala Val Leu Ala Thr Leu Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile						
	90		95		100	105
cag ctg gat cgc ctc ggc atc ctg gaa aag tac ggc gtt gaa ctc atc						1832
Gln Leu Asp Arg Leu Gly Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile						
	110		115		120	
ggt gca gac atc gat gcc att gag cgc ggc gaa gat cgc cag aag ttc						1880
Gly Ala Asp Ile Asp Ala Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe						
	125		130		135	
aag gat att gtc acc acc atc ggt ggc gaa tcc gcg cgt tcc cgc gtc						1928
Lys Asp Ile Val Thr Thr Ile Gly Gly Glu Ser Ala Arg Ser Arg Val						

140	145	150	
tgc tac aac atg gac gaa gtc cat gag act gtc gca gaa ctt ggc ctt			1976
Cys His Asn Met Asp Glu Val His Glu Thr Val Ala Glu Leu Gly Leu			
155	160	165	
cca gta gtc gtg cgt cca tcc ttc act atg ggt ggc ctg ggc tcc ggt			2024
Pro Val Val Val Arg Pro Ser Phe Thr Met Gly Gly Leu Gly Ser Gly			
170	175	180	185
ctt gca tac aac acc gaa gac ctt gag cgc atc gca ggt ggc gga ctt			2072
Leu Ala Tyr Asn Thr Glu Asp Leu Glu Arg Ile Ala Gly Gly Gly Leu			
	190	195	200
gct gca tct cct gaa gca aac gtc ttg atc gaa gaa tcc atc ctt ggt			2120
Ala Ala Ser Pro Glu Ala Asn Val Leu Ile Glu Glu Ser Ile Leu Gly			
	205	210	215
tgg aag gaa ttc gag ctc gag ctc atg cgc gat acc gca gac aac gtt			2168
Trp Lys Glu Phe Glu Leu Glu Leu Met Arg Asp Thr Ala Asp Asn Val			
	220	225	230
gtg gtt atc tgc tcc att gaa aac gtc gac gca ctg ggc gtg cac acc			2216
Val Val Ile Cys Ser Ile Glu Asn Val Asp Ala Leu Gly Val His Thr			
	235	240	245
ggc gac tct gtc acc gtg gca cct gcc ctg acc ctg act gac cgt gaa			2264
Gly Asp Ser Val Thr Val Ala Pro Ala Leu Thr Leu Thr Asp Arg Glu			
	250	255	260
ttc cag aag atg cgc gat cag ggt atc gcc atc atc cgc gag gtc ggc			2312
Phe Gln Lys Met Arg Asp Gln Gly Ile Ala Ile Ile Arg Glu Val Gly			
	270	275	280
gtg gac acc ggt gga tgt aac atc cag ttc gct atc aac cca gtt gat			2360
Val Asp Thr Gly Cys Asn Ile Gln Phe Ala Ile Asn Pro Val Asp			
	285	290	295
ggc cgc atc atc acc att gag atg aac cca cgt gtg tct cgt tcc tcc			2408
Gly Arg Ile Ile Thr Ile Glu Met Asn Pro Arg Val Ser Arg Ser Ser			
	300	305	310
gcg ctg gca tcc aag gca acg ggc ttc cca att gcc aag atg gct gcc			2456
Ala Leu Ala Ser Lys Ala Thr Gly Phe Pro Ile Ala Lys Met Ala Ala			
	315	320	325
aag ctg gct atc gga tac acc ctg gat gag atc acc aac gac atc act			2504
Lys Leu Ala Ile Gly Tyr Thr Leu Asp Glu Ile Thr Asn Asp Ile Thr			
	330	335	340
ggg gaa acc cca gct gcg ttt gag ccc acc atc gac tac gtc gtg gtc			2552
Gly Glu Thr Pro Ala Ala Phe Glu Pro Thr Ile Asp Tyr Val Val Val			
	350	355	360
aag gcc cca cgc ttt gct ttc gag aag ttt gtc ggc gct gat gac act			2600
Lys Ala Pro Arg Phe Ala Phe Glu Lys Phe Val Gly Ala Asp Asp Thr			
	365	370	375
ttg acc acc acc atg aag tcc gtc ggt gag gtc atg tcc ctg ggc cgt			2648
Leu Thr Thr Thr Met Lys Ser Val Gly Glu Val Met Ser Leu Gly Arg			
	380	385	390
aac tac att gca gca ctg aac aag gca ctg cgt tcc ctg gaa acc aag			2696
Asn Tyr Ile Ala Ala Leu Asn Lys Ala Leu Arg Ser Leu Glu Thr Lys			
	395	400	405
cag cag ggt ttc tgg acc aag cct gat gag ttc ttc gca ggg gag cgc			2744
Gln Gln Gly Phe Trp Thr Lys Pro Asp Glu Phe Phe Ala Gly Glu Arg			
	410	415	420
gct acc gat aag gca gct gtt ctg gaa gat ctc aag cgc cca acc gaa			2792
Ala Thr Asp Lys Ala Ala Val Leu Glu Asp Leu Lys Arg Pro Thr Glu			
	430	435	440
ggc cgc ctc tac gac gtt gag ctg gca atg cgc ctt ggc gca agc gtg			2840
Gly Arg Leu Tyr Asp Val Glu Leu Ala Met Arg Leu Gly Ala Ser Val			
	445	450	455
gaa gaa ctc tac gaa gca tct tct att gat cct tgg ttc ctc gcc gag			2888
Glu Glu Leu Tyr Glu Ala Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu			
	460	465	470
ctt gaa gct ctc gtg cag ttc cgc cag aag ctc gtt gac gca cca ttc			2936
Leu Glu Ala Leu Val Gln Phe Arg Gln Lys Leu Val Asp Ala Pro Phe			
	475	480	485
ctc aac gaa gat ctc ctg cgc gaa gca aag ttc atg ggt ctg tcc gac			2984
Leu Asn Glu Asp Leu Leu Arg Glu Ala Lys Phe Met Gly Leu Ser Asp			

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ctg .cag atc gca gcc ctt cgc cca gag ttc gct ggc gaa gac ggc gta				3032
Leu Gln Ile Ala Ala Leu Arg Pro Glu Phe Ala Gly Glu Asp Gly Val				
510	515	520		
cgc acc ttg cgt ctg tcc cta ggc atc cgc cca gta ttc aag act gtc				3080
Arg Thr Leu Arg Leu Ser Leu Gly Ile Arg Pro Val Phe Lys Thr Val				
525	530	535		
gat acc tgt gca gca gag ttt gaa gct aag act ccg tac cac tac tcc				3128
Asp Thr Cys Ala Ala Glu Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser				
540	545	550		
gca tac gag ctg gat cca gca gct gag tct gag gtc gca cca cag act				3176
Ala Tyr Glu Leu Asp Pro Ala Ala Glu Ser Glu Val Ala Pro Gln Thr				
555	560	565		
gag cgt gaa aag gtc ctg atc ttg ggc tcc ggt cca aac ggc atc ggc				3224
Glu Arg Glu Lys Val Leu Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly				
570	575	580	585	
cag ggc atc gag ttc gac tat tcc tgt gtt cac gca gct ctt gag ctc				3272
Gln Gly Ile Glu Phe Asp Tyr Ser Cys Val His Ala Ala Leu Glu Leu				
590	595	600		
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Ser Arg Val Gly Tyr Glu Thr Val Met Val Asn Cys Asn Pro Glu Thr				
605	610	615		
gtg tcc acc gac tac gac acc gct gac cgc ctg tac ttc gag cca ctg				3368
Val Ser Thr Asp Tyr Asp Thr Ala Asp Arg Leu Tyr Phe Glu Pro Leu				
620	625	630		
acc ttc gaa gac gtc atg gag gtc tac cac gct gag gcg cag tcc ggc				3416
Thr Phe Glu Asp Val Met Glu Val Tyr His Ala Glu Ala Gln Ser Gly				
635	640	645		
acc gtc gca ggt gtt atc gtc cag ctt ggt ggc cag act cct ctg ggc				3464
Thr Val Ala Gly Val Ile Val Gln Leu Gly Gly Gln Thr Pro Leu Gly				
650	655	660	665	
ttg gca gat cgt ttg aag aag gct ggc gtc cct gtc att ggt acc tcc				3512
Leu Ala Asp Arg Leu Lys Lys Ala Gly Val Pro Val Ile Gly Thr Ser				
670	675	680		
cca gag gca atc gac atg gct gag gac cgt ggc gag ttc ggt gca ctg				3560
Pro Glu Ala Ile Asp Met Ala Glu Asp Arg Gly Glu Phe Gly Ala Leu				
685	690	695		
ctg aac cgc gag cag ctt cct gct cca gca ttc ggc acc gca acc tct				3608
Leu Asn Arg Glu Gln Leu Pro Ala Pro Ala Phe Gly Thr Ala Thr Ser				
700	705	710		
ttc gaa gag gct cgc aca gta gcc gat gag atc agc tac cca gtg ctg				3656
Phe Glu Glu Ala Arg Thr Val Ala Asp Glu Ile Ser Tyr Pro Val Leu				
715	720	725		
gtt cgc cct tcc tac gtc ttg ggt ggc cgt ggc atg gag att gtc tac				3704
Val Arg Pro Ser Tyr Val Leu Gly Gly Arg Gly Met Glu Ile Val Tyr				
730	735	740	745	
gat gag gct tcc ctc gag gat tac atc aac cgc gca act gag ttg tct				3752
Asp Glu Ala Ser Leu Glu Asp Tyr Ile Asn Arg Ala Thr Glu Leu Ser				
750	755	760		
tct gac cac cca gtg ctg gtt gac cgc ttc ctg gac aac gct att gag				3800
Ser Asp His Pro Val Leu Val Asp Arg Phe Leu Asp Asn Ala Ile Glu				
765	770	775		
atc gac gtc gac gca ctg tgc gac ggc gac gaa gtc tac ctg gcg ggc				3848
Ile Asp Val Asp Ala Leu Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly				
780	785	790		
gtc atg gaa cac atc gag gaa gcc ggc att cac tcc ggt gac tcc gca				3896
Val Met Glu His Ile Glu Glu Ala Gly Ile His Ser Gly Asp Ser Ala				
795	800	805		
tgt gca ctt cct cca atg act ttg ggc gca cag gac atc gag aag gtc				3944
Cys Ala Leu Pro Pro Met Thr Leu Gly Ala Gln Asp Ile Glu Lys Val				
810	815	820	825	
cgc gaa gca acc aag ctg gct ctg ggc atc ggc gta cag ggc ctg				3992
Arg Glu Ala Thr Lys Lys Leu Ala Leu Gly Ile Gly Val Gln Gly Leu				
830	835	840		
atg aac gtc cag tac gca ctc aag gac gac atc ctc tac gtc atc gag				4040
Met Asn Val Gln Tyr Ala Leu Lys Asp Asp Ile Leu Tyr Val Ile Glu				

845	850	855	
gca aac cca cgt gca tcc cgc acc gtg ccg ttc gtc tcc aag gca acg			4088
Ala Asn Pro Arg Ala Ser Arg Thr Val Pro Phe Val Ser Lys Ala Thr			
860	865	870	
ggc gtc aac ctg gcc aag gca gca tcc cgt atc gca gtg ggc gcc acc			4136
Gly Val Asn Leu Ala Lys Ala Ala Ser Arg Ile Ala Val Gly Ala Thr			
875	880	885	
atc aag gat ctc caa gat gag ggc atg att cct acc gag tac gac ggc			4184
Ile Lys Asp Leu Gln Asp Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly			
890	895	900	
ggc tcc ttg cca ctg gac gct cca atc gct gtg aag gaa gca gtg ttg			4232
Gly Ser Leu Pro Leu Asp Ala Pro Ile Ala Val Lys Glu Ala Val Leu			
910	915	920	
ccg ttc aac cgc ttc cgt cgc cca gat gga aag acc ctg gac acc ctg			4280
Pro Phe Asn Arg Phe Arg Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu			
925	930	935	
ctt tcc cca gag atg aag tcc act ggc gag gtc atg ggc ttg gcc aac			4328
Leu Ser Pro Glu Met Lys Ser Thr Gly Glu Val Met Gly Leu Ala Asn			
940	945	950	
aac ttc ggc gct gca tat gca aag gct gaa gct ggc gcc ttt ggt gca			4376
Asn Phe Gly Ala Ala Tyr Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala			
955	960	965	
ttg cca acc gaa ggc acc gtc ttc gtg acc gtg gct aac cgc gac aag			4424
Leu Pro Thr Glu Gly Thr Val Phe Val Thr Val Ala Asn Arg Asp Lys			
970	975	980	
cgc acc ctg atc ctg cca atc cag cgc ctg gcc tgc atg ggc tac aag			4472
Arg Thr Leu Ile Leu Pro Ile Gln Arg Leu Ala Ser Met Gly Tyr Lys			
990	995	1000	
atc ctc gcc acc gaa ggc acc gca ggc atg ctg cgc cgc aac ggc att			4520
Ile Leu Ala Thr Glu Gly Thr Ala Gly Met Leu Arg Arg Asn Gly Ile			
1005	1010	1015	
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Asp Cys Glu Val Val Leu Lys Ala Ser Asp Ile Arg Glu Gly Val Glu			
1020	1025	1030	
ggc aag tcc atc gtg gat cgt atc cgc gaa ggc gaa gtt gac ctc atc			4616
Gly Lys Ser Ile Val Asp Arg Ile Arg Glu Gly Glu Val Asp Leu Ile			
1035	1040	1045	
ctc aac acc cca gct ggt tct gct ggc gct cgc cac gat ggc tac gat			4664
Leu Asn Thr Pro Ala Gly Ser Ala Gly Ala Arg His Asp Gly Tyr Asp			
1050	1055	1060	
atc cgc gca gca gca gtg acc gtg ggt gtt cca ctg atc acc act gtc			4712
Ile Arg Ala Ala Ala Val Thr Val Gly Val Pro Leu Ile Thr Thr Val			
1070	1075	1080	
cag ggt gtc acc gca gct gtc cag ggc att gag gcc ctg cgt gag ggc			4760
Gln Gly Val Thr Ala Ala Val Gln Gly Ile Glu Ala Leu Arg Glu Gly			
1085	1090	1095	
ggt gtc agc gtc cgc gcg ctg cag gaa ctc gac cac gca gtc aag gct			4808
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<210> SEQ ID NO 2
 <211> LENGTH: 393
 <212> TYPE: PRT
 <213> ORGANISM: Brevibacterium lactofermentum
 <400> SEQUENCE: 2

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		20					25					30			
Gly	Phe	Gly	Ala	Ile	Gly	Thr	Thr	Leu	Gly	Glu	Ala	Val	Phe	Thr	Thr
		35				40					45				
Ala	Met	Thr	Gly	Tyr	Gln	Glu	Thr	Met	Thr	Asp	Pro	Ser	Tyr	His	Arg
	50				55				60						
Gln	Ile	Val	Val	Ala	Thr	Ala	Pro	Gln	Ile	Gly	Asn	Thr	Gly	Trp	Asn
65					70				75						80

Asp	Glu	Asp	Asn	Glu	Ser	Arg	Asp	Gly	Lys	Ile	Trp	Val	Ala	Gly	Leu
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Val	Ile	Arg	Asp	Leu	Ala	Ala	Arg	Val	Ser	Asn	Trp	Arg	Ala	Thr	Thr
			100					105					110		
Ser	Leu	Gln	Gln	Glu	Met	Ala	Asp	Gln	Gly	Ile	Val	Gly	Ile	Gly	Gly
		115					120					125			
Ile	Asp	Thr	Arg	Ala	Leu	Val	Arg	His	Leu	Arg	Asn	Glu	Gly	Ser	Ile
	130					135					140				
Ala	Ala	Gly	Ile	Phe	Ser	Gly	Ala	Asp	Ala	Gln	Arg	Pro	Val	Glu	Glu
145				150						155					160
Leu	Val	Glu	Ile	Val	Lys	Asn	Gln	Pro	Ala	Met	Thr	Gly	Ala	Asn	Leu
			165						170					175	
Ser	Val	Glu	Val	Ser	Ala	Asp	Glu	Thr	Tyr	Val	Ile	Glu	Ala	Glu	Gly
			180					185					190		
Glu	Glu	Arg	His	Thr	Val	Val	Ala	Tyr	Asp	Leu	Gly	Ile	Lys	Gln	Asn
	195						200					205			
Thr	Pro	Arg	Arg	Phe	Ser	Ala	Arg	Gly	Val	Arg	Thr	Val	Ile	Val	Pro
	210					215					220				
Ala	Glu	Thr	Pro	Leu	Glu	Asp	Ile	Lys	Gln	Tyr	Asn	Pro	Ser	Gly	Val
225					230					235					240
Phe	Ile	Ser	Asn	Gly	Pro	Gly	Asp	Pro	Ala	Ala	Ala	Asp	Val	Met	Val
			245						250					255	
Asp	Ile	Val	Arg	Glu	Val	Leu	Glu	Ala	Asp	Ile	Pro	Phe	Phe	Gly	Ile
		260						265				270			
Cys	Phe	Gly	Asn	Gln	Ile	Leu	Gly	Arg	Ala	Phe	Gly	Met	Glu	Thr	Tyr
	275						280					285			
Lys	Leu	Lys	Phe	Gly	His	Arg	Gly	Ile	Asn	Val	Pro	Val	Lys	Asn	His
	290					295					300				
Ile	Thr	Gly	Lys	Ile	Asp	Ile	Thr	Ala	Gln	Asn	His	Gly	Phe	Ala	Leu
305					310					315					320
Lys	Gly	Glu	Ala	Gly	Gln	Glu	Phe	Glu	Thr	Asp	Phe	Gly	Thr	Ala	Ile
			325						330					335	
Val	Thr	His	Thr	Cys	Leu	Asn	Asp	Gly	Val	Val	Glu	Gly	Val	Ala	Leu
			340					345					350		
Lys	Ser	Gly	Arg	Ala	Tyr	Ser	Val	Gln	Tyr	His	Pro	Glu	Ala	Ala	Ala
		355					360					365			
Gly	Pro	Asn	Asp	Ala	Ser	Pro	Leu	Phe	Asp	Gln	Phe	Val	Glu	Leu	Met
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<210> SEQ ID NO 3
 <211> LENGTH: 1113
 <212> TYPE: PRT
 <213> ORGANISM: Brevibacterium lactofermentum
 <400> SEQUENCE: 3

Met	Pro	Lys	Arg	Ser	Asp	Ile	Asn	His	Val	Leu	Val	Ile	Gly	Ser	Gly
1				5					10					15	
Pro	Ile	Val	Ile	Gly	Gln	Ala	Cys	Glu	Phe	Asp	Tyr	Ser	Gly	Thr	Gln
		20						25					30		
Ala	Cys	Arg	Val	Leu	Lys	Glu	Glu	Gly	Leu	Arg	Val	Thr	Leu	Ile	Asn
		35				40						45			
Ser	Asn	Pro	Ala	Thr	Ile	Met	Thr	Asp	Pro	Glu	Met	Ala	Asp	His	Thr
	50					55					60				
Tyr	Val	Glu	Pro	Ile	Glu	Pro	Glu	Tyr	Ile	Asp	Lys	Ile	Phe	Ala	Lys
	65				70					75				80	
Glu	Ile	Glu	Gln	Gly	His	Pro	Ile	Asp	Ala	Val	Leu	Ala	Thr	Leu	Gly
			85						90					95	
Gly	Gln	Thr	Ala	Leu	Asn	Ala	Ala	Ile	Gln	Leu	Asp	Arg	Leu	Gly	Ile
		100						105					110		
Leu	Glu	Lys	Tyr	Gly	Val	Glu	Leu	Ile	Gly	Ala	Asp	Ile	Asp	Ala	Ile
		115				120					125				
Glu	Arg	Gly	Glu	Asp	Arg	Gln	Lys	Phe	Lys	Asp	Ile	Val	Thr	Thr	Ile
	130					135					140				
Gly	Gly	Glu	Ser	Ala	Arg	Ser	Arg	Val	Cys	His	Asn	Met	Asp	Glu	Val
145					150					155					160

His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser
 165 170 175
 Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp
 180 185 190
 Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala Asn
 195 200 205
 Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu
 210 215 220
 Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu
 225 230 235 240
 Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val Ala
 245 250 255
 Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln
 260 265 270
 Gly Ile Ala Ile Ile Arg Glu Val Gly Val Asp Thr Gly Gly Cys Asn
 275 280 285
 Ile Gln Phe Ala Ile Asn Pro Val Asp Gly Arg Ile Ile Thr Ile Glu
 290 295 300
 Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala Thr
 305 310 315 320
 Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr
 325 330 335
 Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala Phe
 340 345 350
 Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe
 355 360 365
 Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys Ser
 370 375 380
 Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu Asn
 385 390 395 400
 Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys
 405 410 415
 Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val
 420 425 430
 Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu
 435 440 445
 Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser
 450 455 460
 Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe
 465 470 475 480
 Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg
 485 490 495
 Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg
 500 505 510
 Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu
 515 520 525
 Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe
 530 535 540
 Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala
 545 550 555 560
 Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu Ile
 565 570 575
 Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp Tyr
 580 585 590
 Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr
 595 600 605
 Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr
 610 615 620
 Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met Glu
 625 630 635 640
 Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile Val
 645 650 655
 Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys Lys
 660 665 670
 Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala
 675 680 685

Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu Pro
 690 695 700
 Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Ala Arg Thr Val
 705 710 715 720
 Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val Leu
 725 730 735
 Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu Asp
 740 745 750
 Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu Val
 755 760 765
 Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu Cys
 770 775 780
 Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu Glu
 785 790 795 800
 Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met Thr
 805 810 815
 Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys Leu
 820 825 830
 Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala Leu
 835 840 845
 Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser Arg
 850 855 860
 Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys Ala
 865 870 875 880
 Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp Glu
 885 890 895
 Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp Ala
 900 905 910
 Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg Arg
 915 920 925
 Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys Ser
 930 935 940
 Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr Ala
 945 950 955 960
 Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr Val
 965 970 975
 Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro Ile
 980 985 990
 Gln Arg Leu Ala Ser Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly Thr
 995 1000 1005
 Ala Gly Met Leu Arg Arg Asn Gly Ile Asp Cys Glu Val Val Leu Lys
 1010 1015 1020
 Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp Arg
 1025 1030 1035 1040
 Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly Ser
 1045 1050 1055
 Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Val Thr
 1060 1065 1070
 Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala Val
 1075 1080 1085
 Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala Leu
 1090 1095 1100
 Gln Glu Leu Asp His Ala Val Lys Ala
 1105 1110

<210> SEQ ID NO 4
 <211> LENGTH: 32
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: primer for
 amplifying kanamycin resistant gene of
 Streptococcus faecalis
 <400> SEQUENCE: 4
 cccgttaact gcttgaaacc caggacaata ac

<210> SEQ ID NO 5
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:primer for
amplifying kanamycin resistant gene of
Streptococcus faecalis
<400> SEQUENCE: 5
cccgttaaca tgtacttcag aaaagattag 30

<210> SEQ ID NO 6
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:primer for
amplifying Escherichia coli cloning vector pHSG399
<400> SEQUENCE: 6
gatatctacg tgccgatcaa cgtctc 26

<210> SEQ ID NO 7
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:primer for
amplifying Escherichia coli cloning vector pHSG399
<400> SEQUENCE: 7
aggccttttt ttaaggcagt tattg 25